

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/589,233
Source: IFWOP
Date Processed by STIC: 8/22/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 08/22/2006

PATENT APPLICATION: US/10/589,233

TIME: 14:21:39

Input Set : A:\STERN29.002APC SEQLIST.TXT

Output Set: N:\CRF4\08222006\J589233.raw

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4 <110> APPLICANT: Giannotta, Fabrizio
5     Filee, Patrice
6     Galleni, Moreno
7     Frere, Jean-Marie
8     Joris, Bernard
9     Brans, Alain
10    Ruth, Nadia
12 <120> TITLE OF INVENTION: HYBRID PROTEINS OF ACTIVE-SITE SERINE
13    BETA-LACTAMASE
15 <130> FILE REFERENCE: STERN29.002APC
C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/589,233
C--> 17 <141> CURRENT FILING DATE: 2006-08-10
17 <150> PRIOR APPLICATION NUMBER: PCT/EP2005/050174
18 <151> PRIOR FILING DATE: 2005-01-17
20 <150> PRIOR APPLICATION NUMBER: EP 04075430.1
21 <151> PRIOR FILING DATE: 2001-02-11
23 <160> NUMBER OF SEQ ID NOS: 68
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 858
29 <212> TYPE: DNA
30 <213> ORGANISM: Escherichia coli
32 <400> SEQUENCE: 1
33 ccaatgctta atcagtgagg cacctatctc agcgatctgt ctatttcggt catccatagt 60
34 tgcttgactc cccgtcgtgt agataactac gatacgggag ggcttaccat ctggccccag 120
35 tgctgcaatg ataccgcgag acccacgctc accggctcca gatttatcag caataaacca 180
36 gccagccgga agggccgagc gcagaagtgg tcttgcaact ttatccgcct ccatccagtc 240
37 tattaattgt tgccgggaag ctagagtaag tagttcgcca gttaatagtt tgcgcaacgt 300
38 tgttgccatt gctgcaggca tcgtggtgtc acgctcgctg tttggtatgg cttcattcag 360
39 ctccggttcc caacgatcaa ggcgagttac atgatcccc atgttggtgca aaaaagcggg 420
40 tagctccttc ggtcctccga tcgttgctcag aagtaagttg gccgcagtgt tatcactcat 480
41 ggttatggca gcaactgcata attctcttac tgtcatgcca tccgtaagat gcttttctgt 540
42 gactggtgag tactcaacca agtcattctg agaatagtgt atgcggcgac cgagttgctc 600
43 ttgcccggcg tcaacacggg ataataccgc gccacatagc agaactttaa aagtgtcat 660
44 cattggaaaa cgttcttcgg ggcgaaaact ctcaaggatc ttaccgctgt tgagatccag 720
45 ttcgatgtaa cccactcgtg cacccaactg atcttcagca tcttttactt tcaccagcgt 780
46 ttctgggtga gcaaaaacag gaaggcaaaa tgccgcaaaa aagggaataa gggcgacacg 840
47 gaaatgttga atactcat
858
49 <210> SEQ ID NO: 2
50 <211> LENGTH: 921
51 <212> TYPE: DNA
52 <213> ORGANISM: Bacillus licheniformis
54 <400> SEQUENCE: 2

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55 atgaaattat ggttcagtac tttaaaactg aaaaaggctg cagcagtgtt gcttttctct 60
56 tgcgtcgcgc ttgcaggatg cgctaacaat caaacgaatg cctcgcaacc tgccgagaag 120
57 aatgaaaaga cggagatgaa agatgatttt gcaaaacttg aggaacaatt tgatgcaaaa 180
58 ctccggatct ttgcattgga tacaggatca aaccggacgg tagcgtatcg gccggatgag 240
59 cgttttgctt ttgcttcgac gattaaggct ttaactgtag gcgtgctttt gcaacagaaa 300
60 tcaatagaag atctgaacca gagaataaca tatacacgtg atgatcttgt aaactacaac 360
61 ccgattacgg aaaagcacgt tgatacggga atgacgctca aagagcttgc ggatgcttcg 420
62 ctccgatata gtgacaatgc ggcacagaat ctcatcttta aacaaattgg cggacctgaa 480
63 agtttgaaaa aggaactgag gaagattggt gatgagggtta caaatccga acgattcgaa 540
64 ccagagttaa atgaagtga tccgggtgaa actcaggata ccagtacagc aagagcactt 600
65 gtcacaagcc ttccagcctt tgctcttgaa gataaacttc caagtgaana acgcgagctt 660
66 ttaatcgatt ggatgaaacg aaataccact ggagacgcct taatccgtgc cgggtgtgccg 720
67 gacggttggg aagtggctga taaaactgga gcggcatcat atggaacccg gaatgacatt 780
68 gccatcattt ggccgcaaaa aggagatcct gtcgttcttg cagtattatc cagcagggat 840
69 aaaaaggacg ccaagtatga tgataaactt attgcagagg caacaaagggt ggtaatgaaa 900
70 gccttaaaca tgaacggcaa a                                     921

```

72 <210> SEQ ID NO: 3

73 <211> LENGTH: 975

74 <212> TYPE: DNA

75 <213> ORGANISM: Streptomyces cacaoi

77 <400> SEQUENCE: 3

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78 atgcgtatcc gtccaccg tctgtttctc ctccggcgcg tccgcgcgct cgcctctggt 60
79 ccgctggtgg cctgcggtca ggcgtcgggc tccgagagcg gccagcagcc cggcctcggc 120
80 ggttgcgagg cgagcgca cggctcgggc gacgcccacg agaaggagtt ccgggctgctg 180
81 gagaagaagt tcgacgcca cctggcgctc tacgccatcg acaccgcga cggccaggag 240
82 atcaccaccg gggccgacga gcgttcgccc tacggctcga ccttcaaggc cctccaggcg 300
83 ggcgcgatcc ttgcgcaagt tctccgagac gggcgcggaag tccggcgggg cggcgaggcc 360
84 gacggcatgg acaagggtgg ccaactacgg caggacgcga tctgcccaca ctcaccggtg 420
85 accgagaagc acgtcgcgga cggcatgtcc ctgcgcgagc tgtgcgagcg cgtcgtggcc 480
86 tacagcgaca acaccgcggc caacctgtcc ttcgaccagc tcggcgggcg aaggggctca 540
87 acgcgggtcc tcaagcagct cggcgaccac accacgagca tggaccgcta cgagcaggag 600
88 ctgggctcgg ccgtccccgg cgacccccgg gacaccagca cgcgcgcgcg gttcgccgag 660
89 gacctgcgcg ccttcgccgt cgaggacggc gagaaggccg cctcgcgcgc caacgaccgc 720
90 gagcagctga acgactggat gagcgggagc aggaccggcg acgcgctgat ccgggcccgt 780
91 gtgccgaagg actggaagg ggaggacaag agcggccagg tcaagtacgg caccggaac 840
92 gacatcgccg tcgtccgccc gcccgccgcg gcgcgcatcg tcgtctcggt gatgagccac 900
93 ggcgacaccc aggcgcccga gccgcacgac gagctggtgg ccgaggccgg cctcgtcgtc 960
94 gccgacggtc tgaag                                     975

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96 <210> SEQ ID NO: 4

97 <211> LENGTH: 286

98 <212> TYPE: PRT

99 <213> ORGANISM: Escherichia coli

101 <400> SEQUENCE: 4

```

102 Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
103 1          5          10          15
104 Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
105          20          25          30
106 Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
107          35          40          45

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108 Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
109      50                      55                      60
110 Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
111 65                      70                      75                      80
112 Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
113                      85                      90                      95
114 Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
115                      100                      105                      110
116 Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
117                      115                      120                      125
118 Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
119 130                      135                      140
120 Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
121 145                      150                      155                      160
122 Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
123                      165                      170                      175
124 Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
125                      180                      185                      190
126 Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
127                      195                      200                      205
128 Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
129 210                      215                      220
130 Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
131 225                      230                      235                      240
132 Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
133                      245                      250                      255
134 Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
135                      260                      265                      270
136 Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp
137 275                      280                      285
140 <210> SEQ ID NO: 5
141 <211> LENGTH: 307
142 <212> TYPE: PRT
143 <213> ORGANISM: Bacillus licheniformis
145 <400> SEQUENCE: 5
146 Met Lys Leu Trp Phe Ser Thr Leu Lys Leu Lys Lys Ala Ala Ala Val
147 1      5                      10                      15
148 Leu Leu Phe Ser Cys Val Ala Leu Ala Gly Cys Ala Asn Asn Gln Thr
149      20                      25                      30
150 Asn Ala Ser Gln Pro Ala Glu Lys Asn Glu Lys Thr Glu Met Lys Asp
151      35                      40                      45
152 Asp Phe Ala Lys Leu Glu Glu Gln Phe Asp Ala Lys Leu Gly Ile Phe
153 50      55                      60
154 Ala Leu Asp Thr Gly Thr Asn Arg Thr Val Ala Tyr Arg Pro Asp Glu
155 65      70                      75                      80
156 Arg Phe Ala Phe Ala Ser Thr Ile Lys Ala Leu Thr Val Gly Val Leu
157      85                      90                      95
158 Leu Gln Gln Lys Ser Ile Glu Asp Leu Asn Gln Arg Ile Thr Tyr Thr
159      100                      105                      110

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160 Arg Asp Asp Leu Val Asn Tyr Asn Pro Ile Thr Glu Lys His Val Asp
161      115      120      125
162 Thr Gly Met Thr Leu Lys Glu Leu Ala Asp Ala Ser Leu Arg Tyr Ser
163      130      135      140
164 Asp Asn Ala Ala Gln Asn Leu Ile Leu Lys Gln Ile Gly Gly Pro Glu
165 145      150      155      160
166 Ser Leu Lys Lys Glu Leu Arg Lys Ile Gly Asp Glu Val Thr Asn Pro
167      165      170      175
168 Glu Arg Phe Glu Pro Glu Leu Asn Glu Val Asn Pro Gly Glu Thr Gln
169      180      185      190
170 Asp Thr Ser Thr Ala Arg Ala Leu Val Thr Ser Leu Arg Ala Phe Ala
171      195      200      205
172 Leu Glu Asp Lys Leu Pro Ser Glu Lys Arg Glu Leu Leu Ile Asp Trp
173      210      215      220
174 Met Lys Arg Asn Thr Thr Gly Asp Ala Leu Ile Arg Ala Gly Val Pro
175 225      230      235      240
176 Asp Gly Trp Glu Val Ala Asp Lys Thr Gly Ala Ala Ser Tyr Gly Thr
177      245      250      255
178 Arg Asn Asp Ile Ala Ile Ile Trp Pro Pro Lys Gly Asp Pro Val Val
179      260      265      270
180 Leu Ala Val Leu Ser Ser Arg Asp Lys Lys Asp Ala Lys Tyr Asp Asp
181      275      280      285
182 Lys Leu Ile Ala Glu Ala Thr Lys Val Val Met Lys Ala Leu Asn Met
183      290      295      300
184 Asn Gly Lys
185 305
188 <210> SEQ ID NO: 6
189 <211> LENGTH: 325
190 <212> TYPE: PRT
191 <213> ORGANISM: Streptomyces cacaoi
193 <400> SEQUENCE: 6
194 Met Arg Ile Arg Pro Thr Arg Arg Leu Leu Leu Gly Ala Val Ala Pro
195 1      5      10      15
196 Leu Ala Leu Val Pro Leu Val Ala Cys Gly Gln Ala Ser Gly Ser Glu
197      20      25      30
198 Ser Gly Gln Gln Pro Gly Leu Gly Gly Cys Gly Thr Ser Ala His Gly
199      35      40      45
200 Ser Ala Asp Ala His Glu Lys Glu Phe Arg Ala Leu Glu Lys Lys Phe
201      50      55      60
202 Asp Ala His Pro Gly Val Tyr Ala Ile Asp Thr Arg Asp Gly Gln Glu
203 65      70      75      80
204 Ile Thr His Arg Ala Asp Glu Arg Phe Ala Tyr Gly Ser Thr Phe Lys
205      85      90      95
206 Ala Leu Gln Ala Gly Ala Ile Leu Ala Gln Val Leu Arg Asp Gly Arg
207      100      105      110
208 Glu Val Arg Arg Gly Ala Glu Ala Asp Gly Met Asp Lys Val Val His
209      115      120      125
210 Tyr Gly Gln Asp Ala Ile Leu Pro Asn Ser Pro Val Thr Glu Lys His
211      130      135      140

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```

212 Val Ala Asp Gly Met Ser Leu Arg Glu Leu Cys Asp Ala Val Val Ala
213 145                      150                      155                      160
214 Tyr Ser Asp Asn Thr Ala Ala Asn Leu Leu Phe Asp Gln Leu Gly Gly
215                      165                      170                      175
216 Arg Arg Gly Ser Thr Arg Val Leu Lys Gln Leu Gly Asp His Thr Thr
217                      180                      185                      190
218 Ser Met Asp Arg Tyr Glu Gln Glu Leu Gly Ser Ala Val Pro Gly Asp
219                      195                      200                      205
220 Pro Arg Asp Thr Ser Thr Pro Arg Ala Phe Ala Glu Asp Leu Arg Ala
221                      210                      215                      220
222 Phe Ala Val Glu Asp Gly Glu Lys Ala Ala Leu Ala Pro Asn Asp Arg
223 225                      230                      235                      240
224 Glu Gln Leu Asn Asp Trp Met Ser Gly Ser Arg Thr Gly Asp Ala Leu
225                      245                      250                      255
226 Ile Arg Ala Gly Val Pro Lys Asp Trp Lys Val Glu Asp Lys Ser Gly
227                      260                      265                      270
228 Gln Val Lys Tyr Gly Thr Arg Asn Asp Ile Ala Val Val Arg Pro Pro
229                      275                      280                      285
230 Gly Arg Ala Pro Ile Val Val Ser Val Met Ser His Gly Asp Thr Gln
231                      290                      295                      300
232 Asp Ala Glu Pro His Asp Glu Leu Val Ala Glu Ala Gly Leu Val Val
233 305                      310                      315                      320
234 Ala Asp Gly Leu Lys
235                      325

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238 <210> SEQ ID NO: 7

239 <211> LENGTH: 36

240 <212> TYPE: DNA

241 <213> ORGANISM: Artificial Sequence

243 <220> FEATURE:

244 <223> OTHER INFORMATION: synthetic primer

246 <400> SEQUENCE: 7

247 tcagtttaaca atttcaacaa agaacaacaa aatgct

36

249 <210> SEQ ID NO: 8

250 <211> LENGTH: 30

251 <212> TYPE: DNA

252 <213> ORGANISM: Artificial Sequence

254 <220> FEATURE:

255 <223> OTHER INFORMATION: synthetic primer

257 <400> SEQUENCE: 8

258 tcgaaatttt ttgttgtctt cctcttttgg

30

260 <210> SEQ ID NO: 9

261 <211> LENGTH: 33

262 <212> TYPE: DNA

263 <213> ORGANISM: Artificial Sequence

265 <220> FEATURE:

266 <223> OTHER INFORMATION: synthetic primer

268 <400> SEQUENCE: 9

269 catatgaaaa agaaaaacat ttattcaatt cgt

33

271 <210> SEQ ID NO: 10

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/589,233

DATE: 08/22/2006

TIME: 14:21:40

Input Set : A:\STERN29.002APC SEQLIST.TXT

Output Set: N:\CRF4\08222006\J589233.raw

L:17 M:270 C: Current Application Number differs, Replaced Current Application No

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date